

## FIG. 1

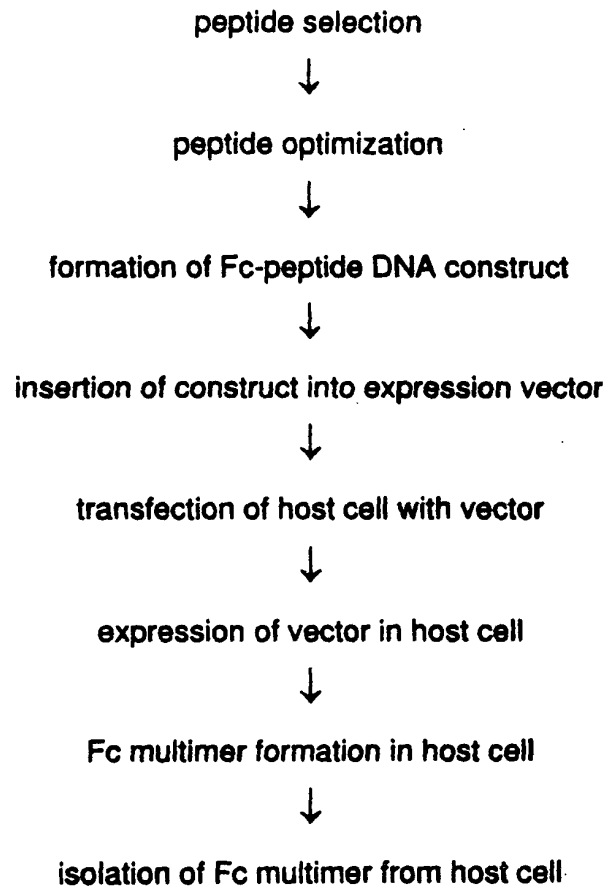


FIG. 2A

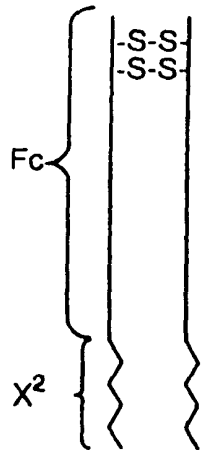


FIG. 2B

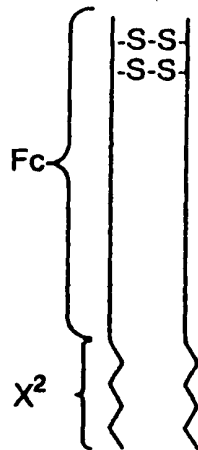


FIG. 2C

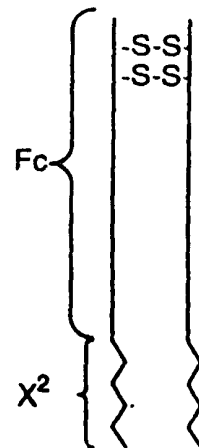


FIG. 2D

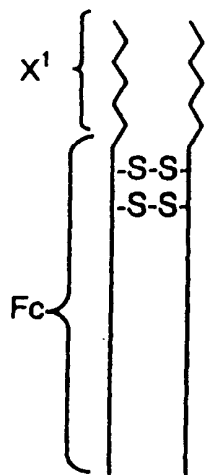


FIG. 2E

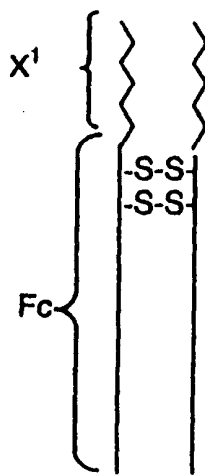


FIG. 2F

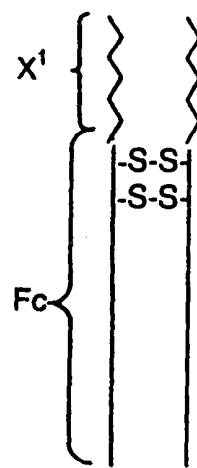


FIG. 3A



FIG. 3B

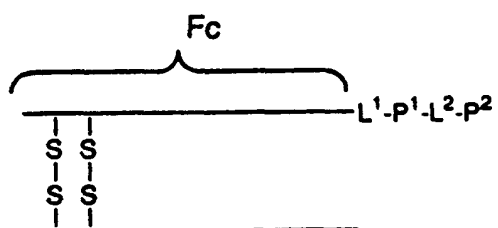
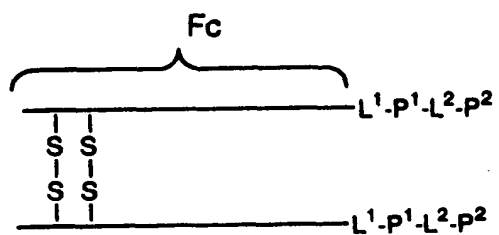


FIG. 3C



# FIG. 4

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ATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCCTGGGGGGACCGTCA
1  -----+-----+-----+-----+-----+-----+-----+-----+ 60
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCCTTGAGGACCCCCCTGGCAGT

a      M D K T H T C P P C P A P E L L G G P S

GTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
61  -----+-----+-----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

a      V F L F P P K P K D T L M I S R T P E V

ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a      T C V V V D V S H E D P E V K F N W Y V

GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGG
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

a      D G V E V H N A K T K P R E E Q Y N S T

TACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTCATG

a      Y R V V S V L T V L H Q D W L N G K E Y

AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
TTCACGTTCCAGAGGTTGTTTCGGGAGGGTTCGGGGTAGCTCTTTTGGTAGAGGTTTCGG

a      K C K V S N K A L P A P I E K T I S K A

AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG

a      K G Q P R E P Q V Y T L P P S R D E L T

AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a      K N Q V S L T C L V K G F Y P S D I A V

GAGTGGGAGAGCAATGGGCAGCCGGAACAACATAAGACCACGCCTCCCGTGCTGGAC
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
CTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGACGACCTG

a      E W E S N G Q P E N N Y K T T P P V L D

TCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a      S D G S F F L Y S K L T V D K S R W Q Q

GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC

a      G N V F S C S V M H E A L H N H Y T Q K

AGCCTCTCCCTGTCTCCGGGTAAA
661 -----+-----+-----+-----+-----+-----+-----+-----+ 684
TCGGAGAGGGACAGAGGCCCATTT

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FIG. 5

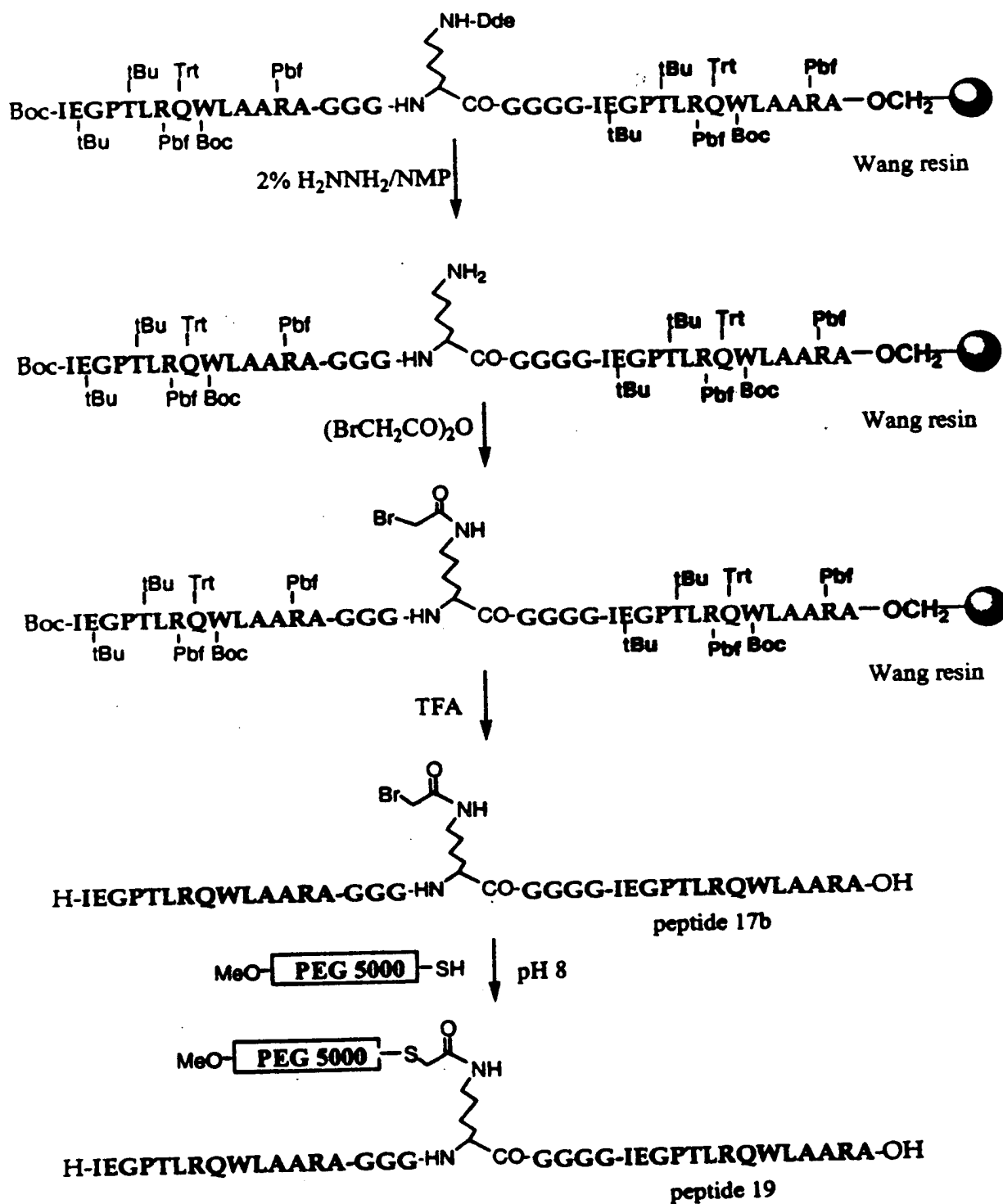
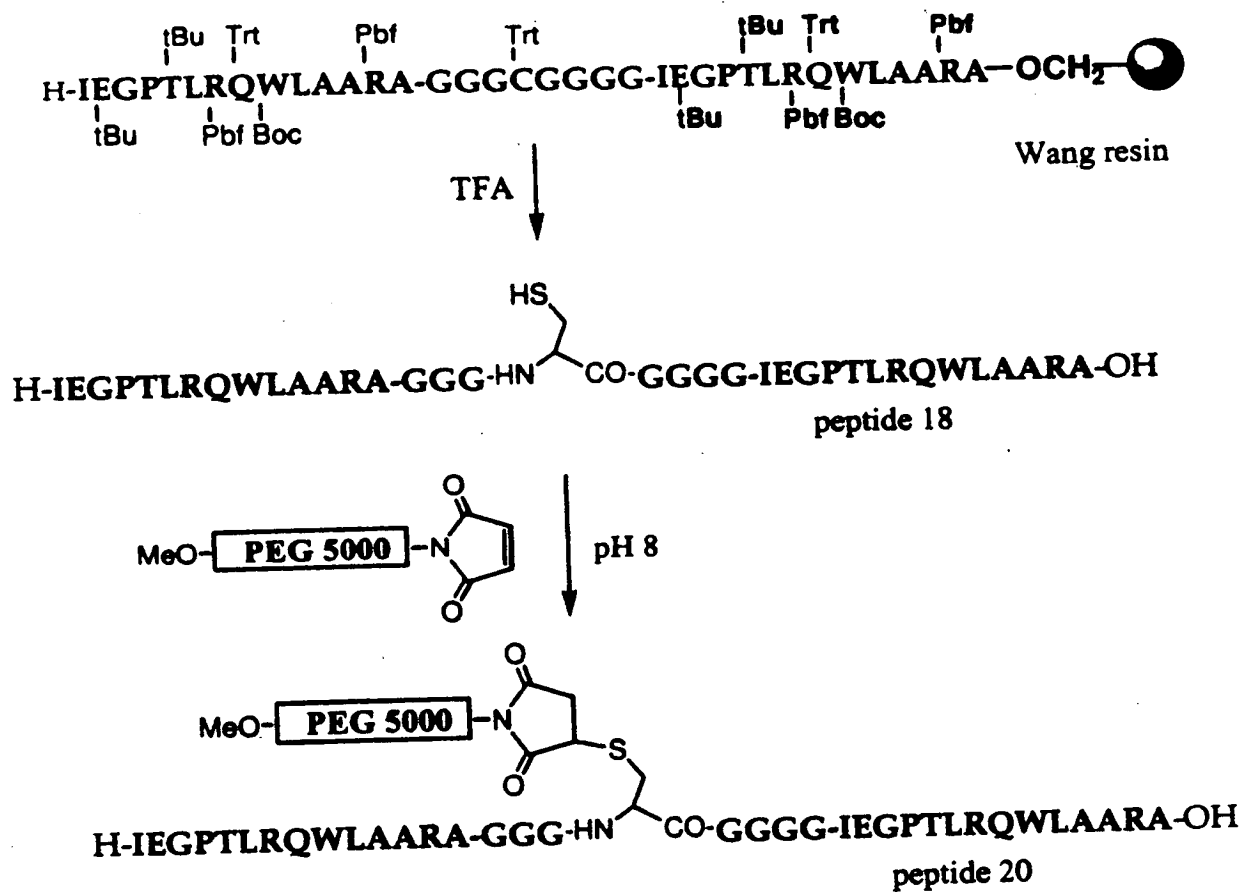


FIG. 6





**С А \* -**





## FIG. 10

XbaI  
|  
TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGATCGAAGGTCCGACTCTGC  
1 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 60  
AGATCTAAACAAAATTGATTAATTCCTCCTTATTGTATACTAGCTTCCAGGCTGAGACG  
M I E G P T L R .  
c  
GTCAGTGGCTGGCTGCTCGTGGTGGAGGCGGTGGGGACAAAACACACATGTCCAC  
61 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 120  
CAGTCACCGACCGACGAGCACGACCACCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTG  
Q W L A A R A G G G G G D K T H T C P P .  
c  
CTTGCCCAGCACCTGAACCTCCTGGGGGACCGTCAGTTTTCTCTTCCCCCAAAAACCA  
121 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 180  
GAACGGGTGCTGGACTTGAGGACCCCCCTGGCAGTCAAAGGAGAAGGGGGTTTTGGGT  
C P A P E L L G G P S V F L F P P K P K .  
c  
AGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCC  
181 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 240  
TCCTGTGGGAGTACTAGAGGGCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG  
D T L M I S R T P E V T C V V V D V S H .  
c  
ACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCA  
241 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 300  
TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT  
E D P E V K F N W Y V D G V E V H N A K .  
c  
AGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAGCGTCTCACCG  
301 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 360  
TCTGTTTCGGCGCCCTCCTCGTCATGTTGTGTCATGGCACACCAGTCGCAGGAGTGGC  
T K P R E E Q Y N S T Y R V V S V L T V .  
c  
TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCC  
361 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 420  
AGGACGTGGTCTCTGACCGACTTACCGTTCTCATGTTACGTTCCAGAGGTGTTTCGGG  
L H Q D W L N G K E Y K C K V S N K A L .  
c  
TCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGG  
421 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 480  
AGGGTCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCC  
P A P I E K T I S K A K G Q P R E P Q V .  
c  
TGTACACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCC  
481 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 540  
ACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGG  
Y T L P P S R D E L T K N Q V S L T C L .  
c  
TGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGG  
541 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 600  
ACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCC  
V K G F Y P S D I A V E W E S N G Q P E .  
c  
AGAACAACATAAGACCACGCCCTCCCGTGGTGGACTCCGACGGCTCCTTCTTCTCTACA  
601 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 660  
TCTTGTGATGTTCTGGTGGGAGGGCAGGACCTGAGGCTGCCGAGGAAGAAGGAGATGT  
N N Y K T T P P V L D S D G S F F L Y S .  
c  
GCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA  
661 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 720  
CGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGCACT  
K L T V D K S R W Q Q G N V F S C S V M .  
c  
TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAT  
721 .....+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 780  
ACGTACTCCGAGACGTGTTGGTGTGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTA  
H E A L H N H Y T Q K S L S L S P G K .  
c  
BamHI  
|  
AATGGATCC  
781 ..... 789  
TTACCTAGG

FIG.11

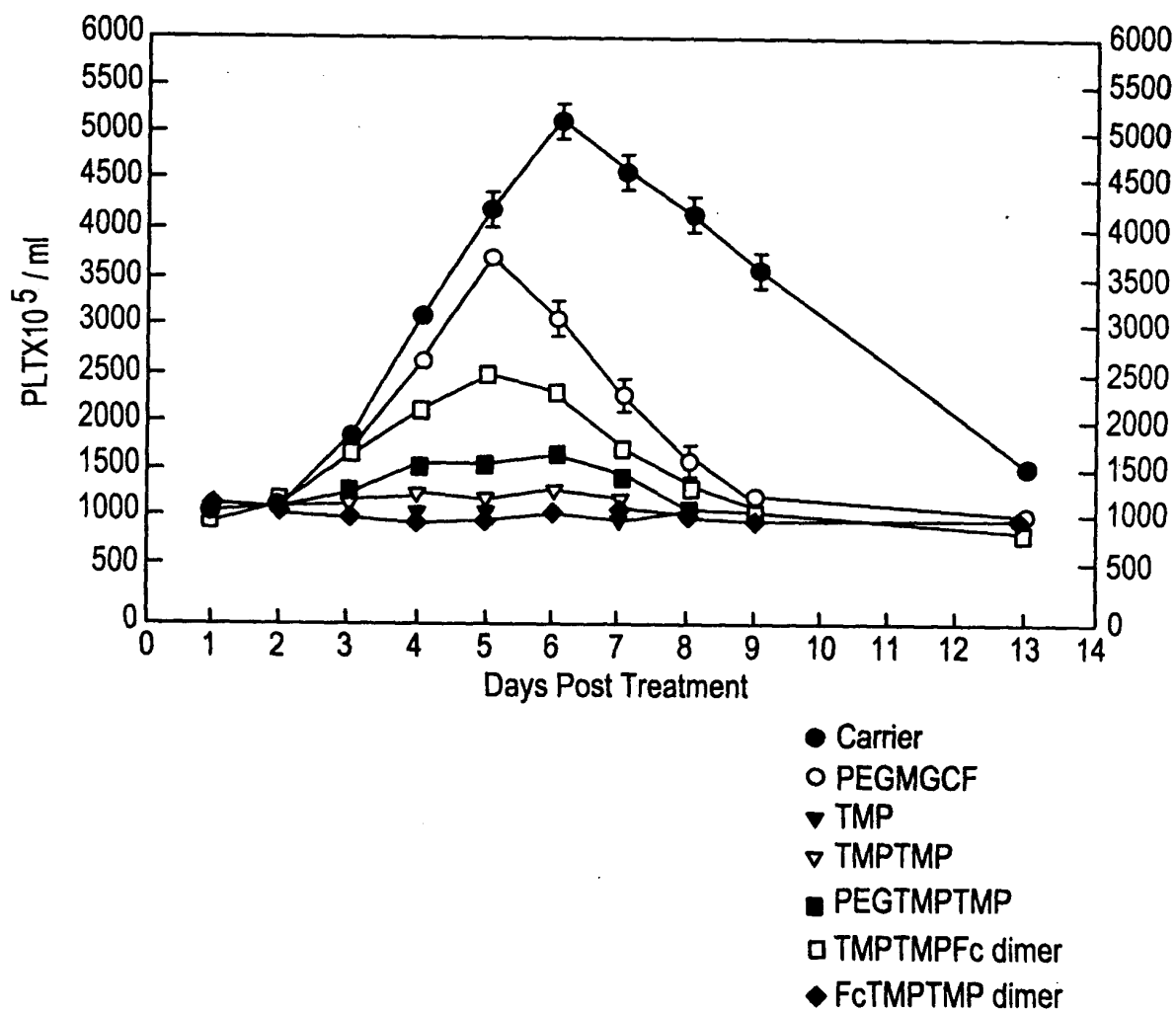
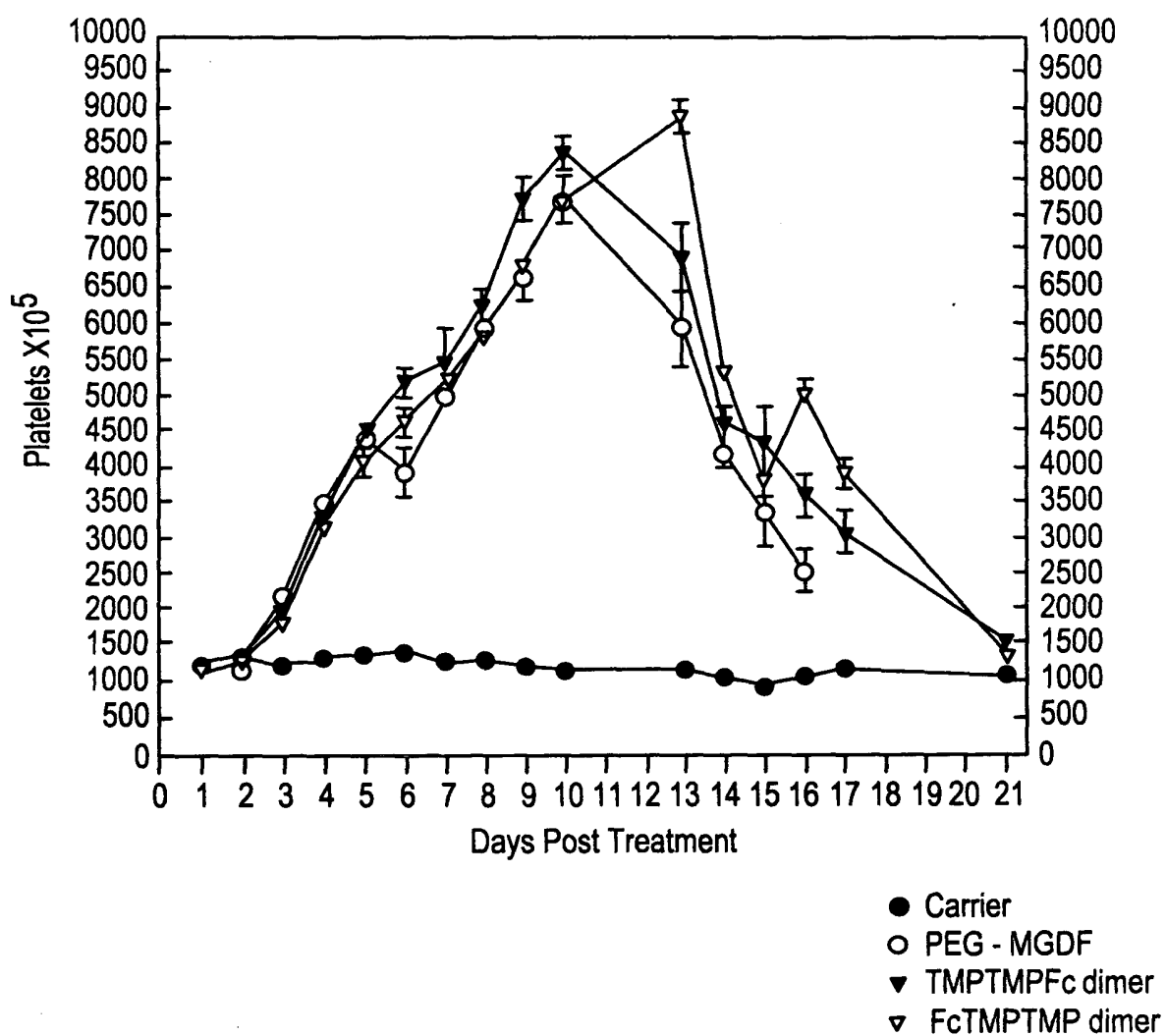


FIG.12



XbaI  
|

1 TCTAGATTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACCTCACACATGTC 60  
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTGTTTTGAGTGTGTACAG  
CACCTTGTCCAGCTCCGGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAAC  
61 GTGGAACAGGTCGAGGCCTTGAGGACCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTG 120  
P C P A P E L L G G P S V F L F P P K P  
CCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA  
121 GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCAC 180  
K D T L M I S R T P E V T C V V V D V S  
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG  
181 CCGTGTCTTCTGGGACTCCAGTTCAAGTTGACCATTGCACCTGCCGCACCTCCACGTATTAC 240  
H E D P E V K F N W Y V D G V E V H N A  
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCA  
241 GGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGT 300  
K T K P R E E Q Y N S T Y R V V S V L T  
CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAG  
301 GGCAGGACGTGGTCTTGACCGACTTACCGTTCTCTCATGTTTACGTTCCAGAGGTTGTTT 360  
V L H Q D W L N G K E Y K C K V S N K A  
CCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC  
361 GGGAGGGTTCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG 420  
L P A P I E K T I S K A K G Q P R E P Q  
AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT  
421 TCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGA 480  
V Y T L P P S R D E L T K N Q V S L T C  
GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC  
481 CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCP 540  
L V K G F Y P S D I A V E W E S N G Q P  
CGGAGAACAAC TACAAGACCACGCCTCCCGTGTGACTCCGACGGCTCTTCTCTCTCT  
541 GCCTCTTGTGTGATGTTCTGGTGGGAGGGACGACCTGAGGCTGCCGAGGAAGAAGGAGA 600  
E N N Y K T T P P V L D S D G S F F L Y  
ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG  
601 TGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCCTCGTCCCTTGCAGAAGAGTACGAGGC 660  
S K L T V D K S R W Q Q G N V F S C S V  
TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA  
661 ACTACGTA TCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT 720  
M H E A L H N H Y T Q K S L S L S P G K  
AAGGTGGAGGTGGTGGTGGAGGTACTTACTCTTGCCACTTCGGCCCGCTGACTTGGGTTT  
721 TTCCACCTCCACCACCACCTCCATGAATGAGAACGGTGAAGCCGGGCGACTGAACCCAAA 780  
G G G G G G G T Y S C H F G P L T W V C  
BamHI  
|

781 GCAAACCGCAGGGTGGTTAATCTCGTGGATCC 812  
CGTTTGGCGTCCCACCAATTAGAGCACCTAGG  
K P O G G \*

## FIG. 14

XbaI  
|  
1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGGAGGTACTTACTCTTGCC 60  
AGATCTAAACAAAATTGATTAATTTCTCTCTTATTGTATACCTCCATGAATGAGAACGG  
M G G T Y S C H  
c  
61 ACTTCGGCCCCGCTGACTTGGGTATGTAAGCCACAAGGGGTGGGGGAGCGGGGGGGACA 120  
TGAAGCCGGGCGACTGAACCCATACATTGGGTGTTCCCCACCCCTCCGCCCCCTGT  
F G P L T W V C K P Q G G G G G G G D K  
c  
121 AAACCTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTC 180  
TTTGAGTGTGTACAGGTGGAACGGGTGCGTGGACTTGAGGACCCCTGGCAGTCAAAAGG  
T H T C P P C P A P E L L G G P S V F L  
c  
181 TCTTCCCCCAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCG 240  
AGAAGGGGGGTTTGGGTTCCTGTGGGAGTACTAGAGGGCTGGGGACTCCAGTGTACGC  
F P P K P K D T L M I S R T P E V T C V  
c  
241 TGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCG 300  
ACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCCG  
V V D V S H E D P E V K F N W Y V D G V  
c  
301 TGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG 360  
ACCTCCACGTATTACGGTTCGTTCGGCGCCCTCCTCGTCATGTTGTCGTGTCATGGCAC  
E V H N A K T K P R E E Q Y N S T Y R V  
c  
361 TGGTCAGCGTCTCACCCTGCTGACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA 420  
ACCACTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCTCATGTTTCACGT  
V S V L T V L H Q D W L N G K E Y K C K  
c  
421 AGGTCTCCAAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGC 480  
TCCAGAGGTGTTTCGGGAGGGTCCGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCG  
V S N K A L P A P I E K T I S K A K G Q  
c  
481 AGCCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACC 540  
TCGGGGCTCTTGGTGTCCACATGTGGACGGGGTAGGGCCCTACTCGACTGGTCTTGG  
P R E P Q V Y T L P P S R D E L T K N Q  
c  
541 AGGTCAAGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG 600  
TCCAGTCGGACTGGACGGACCAAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCC  
V S L T C L V K G F Y P S D I A V E W E  
c  
561 AGAGCAATGGGCAGCCGGAGAACAACATAAGACCACGCCTCCCGTGTGGACTCCGACG 660  
TCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGACGACCTGAGGCTGC  
S N G Q P E N N Y K T T P P V L D S D G  
c  
661 GCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCGGGAACG 720  
CGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGC  
S F F L Y S K L T V D K S R W Q Q G N V  
c  
721 TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCT 780  
AGAAGAGTACGAGGCACTACTCTCCGAGACGTGTTGGTGTATGTGCGTCTTCTCGGAGA  
F S C S V M H E A L H N H Y T Q K S L S  
c  
BamHI  
|  
781 CCCTGTCTCCGGGTAAATAATGGATCC 807  
GGGACAGAGGCCCATTTATTACCTAGG  
L S P G K \*

# FIG. 15

XbaI  
 |  
 1 TCTAGATTTGAGTTTAACTTTTGAAGGAGGAATAAAATATGGGAGGTACTTACTCTTG 60  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 AGATCTAAACTCAAATTGAAAATCTTCTCTTATTTTATACCCTCCATGAATGAGAAC  
 b M G G T Y S C -

61 CCACTTCGGCCCACTGACTTGGGTTTGCAAACCGCAGGGTGGCGGCGGCGGCGGCGGTGG 120  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b GGTGAAGCCGGGTGACTGAACCCAAACGTTTGGCGTCCACCGCGCGCGCGCGCGCCACC  
 H F G P L T W V C K P Q G G G G G G G G -

121 TACCTATTCTGTCTATTTGGCCCGCTGACCTGGGTATGTAAGCCACAAGGGGTGGGGG 180  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b ATGGATAAGGACAGTAAAACCGGCGGACTGGACCCATACATTCGGTGTTCCTCCACCCCC  
 T Y S C H F G P L T W V C K P Q G G G G -

181 AGGCGGGGGGACAAAACCTCACACATGTCCACCTTGCCACGACCTGAACTCCTGGGGGG 240  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b TCCGCCCCCCTGTTTGGAGTGTGTACAGGTGGAACGGGTGCTGGACTTGAGGACCCCC  
 G G G D K T H T C P P C P A P E L L G G -

241 ACCGTCAGTTTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCC 300  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b TGGCAGTCAAAGGAGAAGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGG  
 P S V F L P P P K P K D T L M I S R T P -

301 TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTG 360  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b ACTCCAGTGACGACCAACCACTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGAC  
 E V T C V V V D V S H E D P E V K P N W -

361 GTACGTGGACGGCTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAA 420  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b CATGCACCTGCCGACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCTCGTCATGTT  
 Y V D G V E V H N A K T K P R E E Q Y N -

421 CAGCACGTACCGTGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAA 480  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b GTCGTGCATGGCACACCACTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTT  
 S T Y R V V S V L T V L H Q D W L N G K -

481 GGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTC 540  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b CCTCATGTTACGTTCCAGAGGTGTTTTCGGGAGGGTGGGGGTAGCTCTTTTGGTAGAG  
 E Y K C K V S N K A L P A P I E K T I S -

541 CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGA 600  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b GTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACT  
 K A K G Q P R E P Q V Y T L P P S R D E -

601 GCTGACCAAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT 660  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b CGACTGGTTCTTGGTCCAGTCCGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTA  
 L T K N Q V S L T C L V K G F Y P S D I -

661 CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACCTACAAGACCACGCTCCCGT 720  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b GCGGCACCTCACCTCTCTGTTACCCGTGCGCTCTTGTGTATGTTCTGGTGGGAGGGCA  
 A V E W E S N G Q P E N N Y K T T P P V -

721 GCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTG 780  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b CGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTTCTCGTCCAC  
 L D S D G S F F L Y S K L T V D K S R W -

781 GCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACAC 840  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b CGTCGTCCCCTTGCAAGAGTACGAGGCACTACGTACTCCGAGACGTGTGGTGTATGTG  
 Q Q G N V F S C S V M H E A L H N H Y T -

BamHI  
 |  
 841 GCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC 881  
 .....+.....+.....+.....+.....+.....+.....+.....+.....+  
 b CGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG  
 Q K S L S L S P G K \*

## FIG. 16

XbaI  
|  
1 TCTAGATTTGTTTAACTAATTAAAGGAGGAATAACATATGGACAAAACTCACACATGTC 60  
AGATCTAAACAAAATTGATTAATTTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAG  
M D K T H T C P -  
c  
61 CACCTTGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTTTTCTCTTCCCCCAAAC 120  
GTGGAACGGGTCGTGGACTTGAGGACCCCTGGCAGTCAAAAGGAGAAGGGGGTTTTG  
P C P A P E L L G G P S V F L P P K P -  
c  
121 CCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGA 180  
GGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACT  
K D T L M I S R T P E V T C V V V D V S -  
c  
181 GCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTGCATAATG 240  
CGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC  
H E D P E V K F N W Y V D G V E V H N A -  
c  
241 CCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCA 300  
GGTTCGTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCGTCGAGGAGT  
K T K P R E E Q Y N S T Y R V V S V L T -  
c  
301 CCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG 360  
GGCAGGACGTGGTTCCTGACCGACTTACCGTTCTCTCATGTTACGTTCCAGAGGTTGTTTC  
V L H Q D W L N G K E Y K C K V S N K A -  
c  
361 CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC 420  
GGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTG  
L P A P I E K T I S K A K G Q P R E P Q -  
c  
421 AGGTGTACACCCCTGCCTCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCTGACCT 480  
TCCACATGTGGGACGGAGGTAGGGCCCTACTCGACTGGTCTTGGTCCAGTCGGACTGGA  
V Y T L P P S R D E L T K N Q V S L T C -  
c  
481 GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC 540  
CGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCG  
L V K G F Y P S D I A V E W E S N G Q P -  
c  
541 CGGAGAACAACACTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCT 600  
GCCTCTTGTGATGTTCTGGTGGGAGGGACGACCTGAGGCTGCCGAGGAAGAAGGAGA  
E N N Y K T T P P V L D S D G S F F L Y -  
c  
601 ACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG 660  
TGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAAGAGTACGAGGC  
S K L T V D K S R W Q Q G N V F S C S V -  
c  
661 TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA 720  
ACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCAT  
M H E A L H N H Y T Q K S L S L S P G K -  
c  
721 AAGGTGGAGGTGGTGGCGGAGGTACTTACTTGTCCACTTCGGCCCACTGACTTGGGTTT 780  
TTCCACCTCCACCACCGCTCATGAATGAGAACGGTGAAGCCGGGTGACTGAACCCAAA  
G G G G G G G T Y S C H F G P L T W V C -  
c  
781 GCAAACCGCAGGGTGGCGGCGGCGGCGGCGGTGACCTATTCTGTCTATTTGGCCCCG 840  
CGTTTGGCGTCCACCGCCGCGCGCGCCGACCATGGATAAGGACAGTAAACCGGGCG  
K P Q G G G G G G G T Y S C H F G P L -  
c  
BamHI  
|  
841 TGACCTGGGTATGTAAGCCACAAGGGGGTTAATCTCGAGGATCC 884  
ACTGGACCCATACATTGGTGTTCCTCCCAATTAGAGCTCCTAGG  
T W V C K P Q G G -



## FIG. 17A

[AatII sticky end]  
(position #4358 in pAMG21)

5' GCGTAACGTATGCATGGTCTCC -  
3' TGCACGCATTGCATACGTACCAGAGG -

- CCATGCGAGAGTAGGGAAC TGCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT -  
- GGTACGCTCTCATCCCTTGACGGTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGA -

- GGGCCTTTCGTTTTATCTGTTGTTGTGCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC -  
- CCCGAAAGCAAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCCTGTTTAGGCG -

- CGGGAGCGGATTTGAACGTTGCGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCCG -  
- GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCCCTCCACCGCCCGTCTGCGGGCG -

- CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTGCGT -  
- GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA -

AatII

- TTCTACAAACTCTTTTGTTTATTTTCTAAATACATTCAAATATGGACGTCGTACTTAAC -  
- AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG -

- TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAATTGCTTTAGAAATACTTTGGCAGC -  
- AAAATTTACATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG -

- GGTGTTGTTGATTGAGTTTCATTTGCGCATTGGTTAAATGGAAAGTGACCGTGCGCTTAC -  
- CCAACAACATAACTCAAAGTAAACGCGTAACCAATTTACCTTTCACTGGCAGCGGAATG -

- TACAGCCTAATATTTTTGAAATATCCCAAGAGCTTTTTCCTTCGCATGCCACGCTAAAC -  
- ATGTCGGATTATAAAAACCTTTATAGGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTG -

- ATTCTTTTTCTCTTTTGTTTAAATCGTTGTTTGATTTATTATTTGCTATATTTATTTTC -  
- TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAATAAAAAG -

- GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAAAAATA -  
- CTATTAATAGTTGATCTCTTCCTTGTTAATTACCATACAAGTATGTGCGTACATTTTTAT -

- AACTATCTATATAGTTGTCTTTCTCTGAATGTGCAAAACTAAGCATTCCGAAGCCATTAT -  
- TTGATAGATATATCAACAGAAAGAGACTTACACGTTTTGATTTCGTAAGGCTTCGGTAATA -

- TAGCAGTATGAATAGGGAAC TAAACCCAGTGATAAGACCTGATGATTTTCGCTTCTTTAA -  
- ATCGTCATACTTATCCCTTTGATTTGGGTCACTATTCTGGACTACTAAAGCGAAGAAAT -

- TTACATTTGGAGATTTTATTTTACAGCATTGTTTTCAAATATATTCCAATTAATCGGTG -  
- AATGTAAACCTCTAAAAATAAATGTCGTAACAAAAGTTTATATAAGGTTAATTAGCCAC -

- AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT -  
- TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAATAATTTAATCGCAGTAGTA -

- AATATTGCCTCCATTTTATAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG -  
- TTATAACGGAGGTAAAAATCCCATTAATAGGTCTTAACCTTTATAGTCTAAATTGGTATC -

- AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG -  
- TTACTCCTATTTACTAGCGCTCATTATTATAAGTGTTACATGGTAAATCAGTATAGTC -

- ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT -  
- TATTCCGTAAC TAATTATAGTAATAACGAAGATGTCCGAAATTAAAAATAATTAATAAGACA -

- AAGTGTCGTCGGCATTATGTCTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTG -  
- TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG -

- GCAAGTTTTGCGTGTTATATATCATTTAAACGGTAATAGATTGACATTTGATTCTAATAA -  
- CGTTCAAACGCACAATATATAGTAATTTTGCCATTATCTAACTGTAACTAAGATTATT -

## FIG. 17B

- ATTGGATTTTGTGCACACTATTATATCGCTTGAAATACAATTGTTTAACATAAGTACCTG -  
- TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC -  
- TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTGATT -  
- ATCCTAGCATGTCCAAATGCGTTCTTTTACCAAACAATATCAGCTAATTAGCTAAACTAA -  
- CTAGATTTGTTTTAACTAATTAAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGA -  
- GATCTAAACAAAATTGATTAATTTCTCCTTATTGTATACCAATTGCGCAACCTTAAGCT -  
- GCTCACTAGTGTGCGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA -  
- CGAGTGATCACAGCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTTCTT -  
- GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA -  
- CTTCTTCTTCTTCTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGCGGACTCGTTAT -  
- ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTTGCTGAAAGGAGG -  
- TGATCGTATTGGGGAACCCCGGAGATTGCCCAGAACTCCCCAAAAACGACTTTCCTCC -  
- AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end]  
- TTGGCGAGAAGTGCGAGAAGTG 5' (position #5904 in pAMG21)

FIG.18A - 1

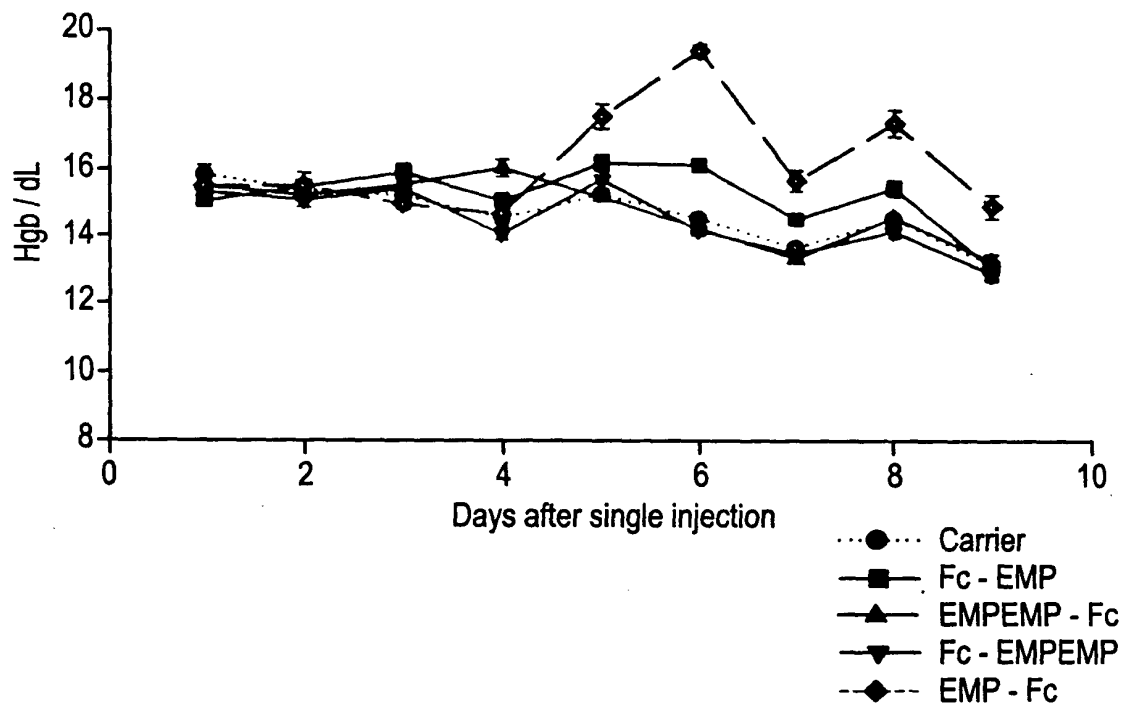


FIG.18A - 2

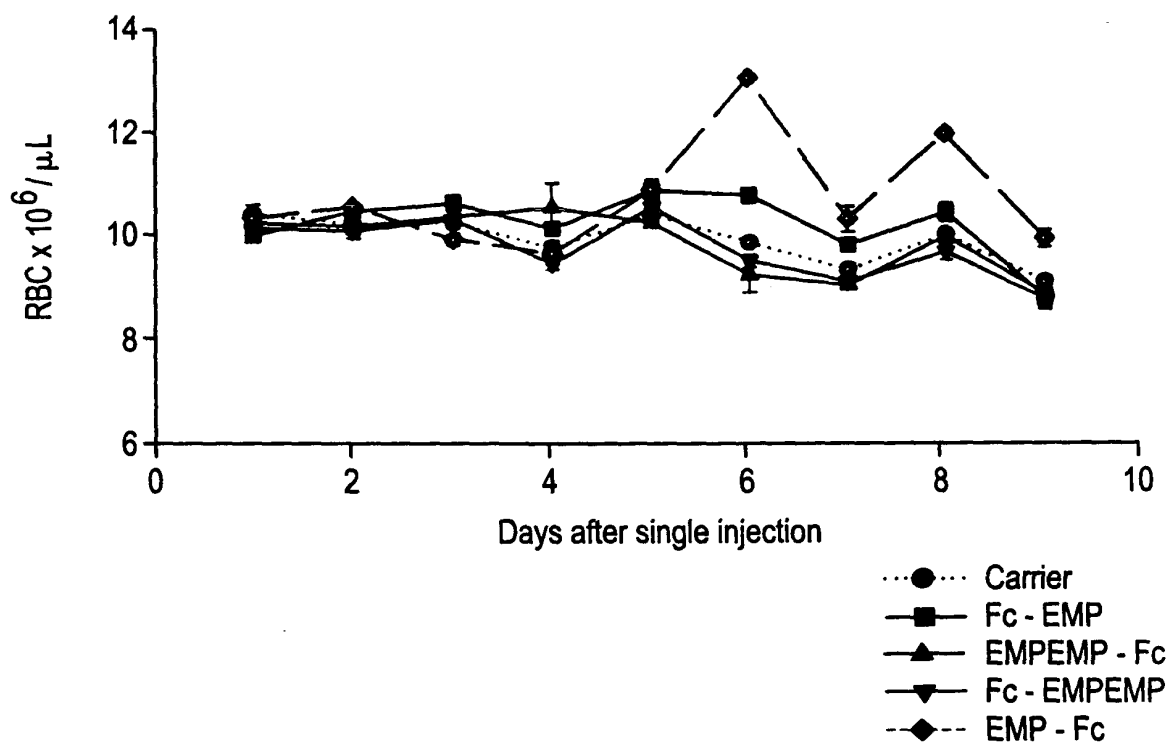


FIG.18A - 3

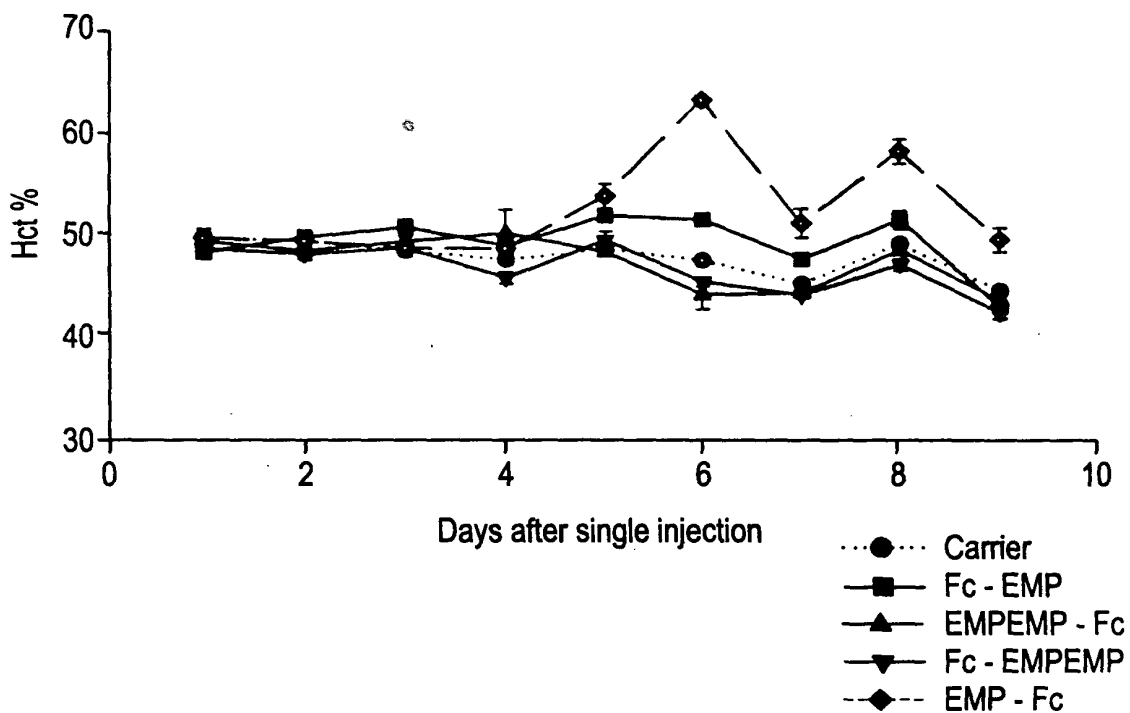


FIG.18B - 1

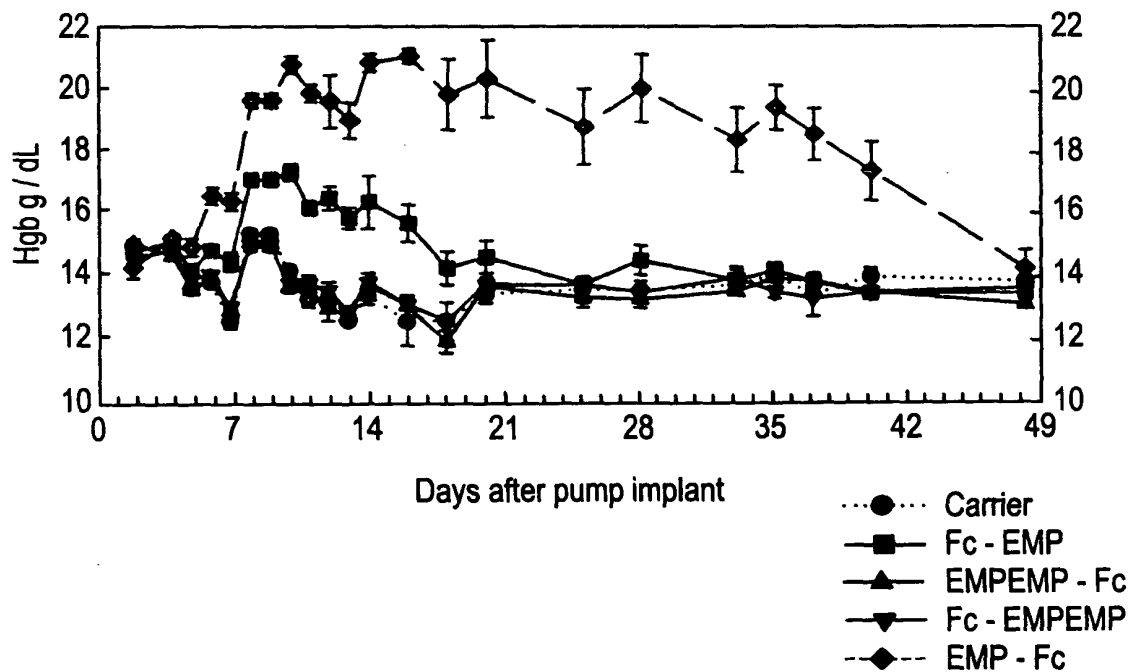


FIG.18B - 2

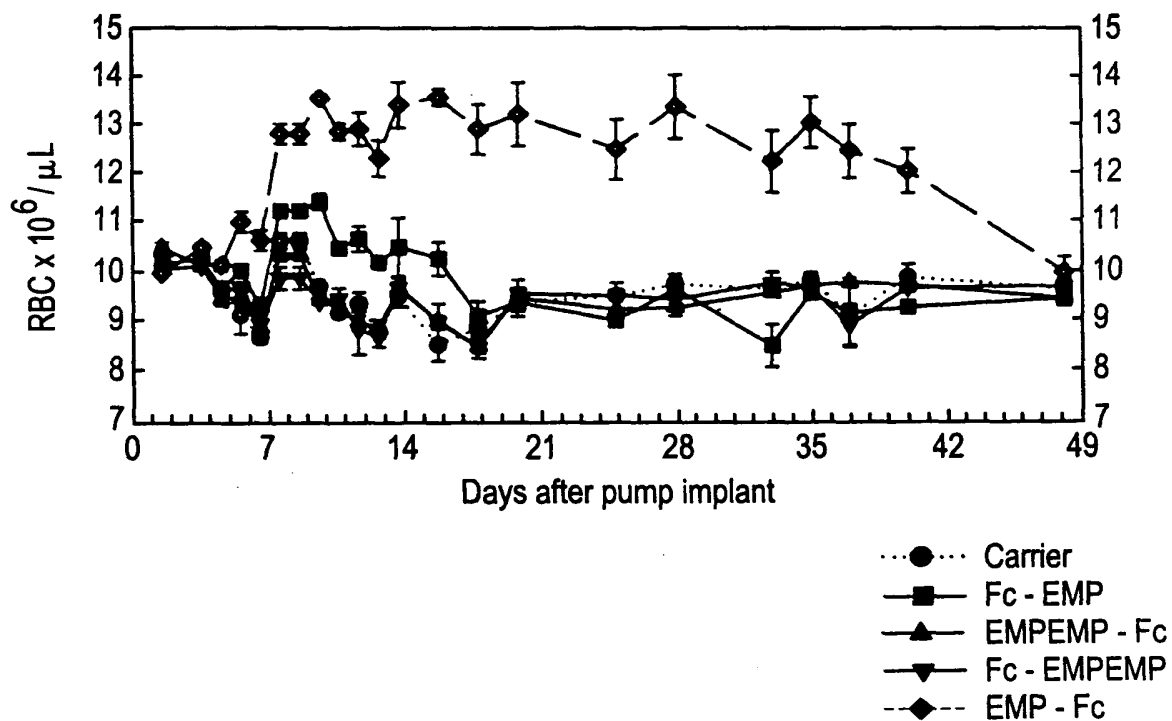
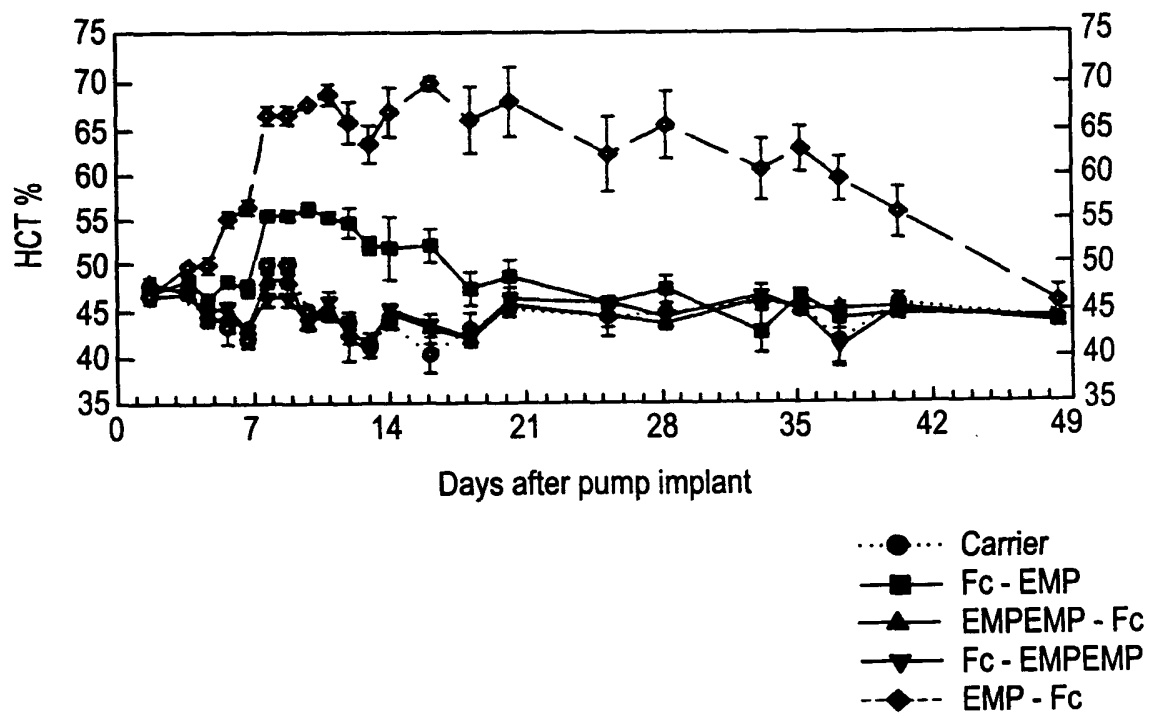


FIG.18B - 3



## FIG. 19A

NdeI  
|  
1 CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG  
-----+-----+-----+-----+-----+-----+-----+ 60  
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC  
a M D K T H T C P P C P A P E L L G G P -  
TCAGTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  
61 -----+-----+-----+-----+-----+-----+-----+ 120  
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
121 -----+-----+-----+-----+-----+-----+-----+ 180  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
181 -----+-----+-----+-----+-----+-----+-----+ 240  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTCGGCGCCCTCCTCGTCATGTTGTGC  
a V D G V E V H N A K T K P R E E Q Y N S -  
ACGTACCGTGTGGTCAGCGTCCCTACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
241 -----+-----+-----+-----+-----+-----+-----+ 300  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCCTGACCGACTTACCGTTCCCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA  
301 -----+-----+-----+-----+-----+-----+-----+ 360  
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
361 -----+-----+-----+-----+-----+-----+-----+ 420  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC  
421 -----+-----+-----+-----+-----+-----+-----+ 480  
TGTTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACCTACAAGACCACGCCTCCCGTGCTG  
481 -----+-----+-----+-----+-----+-----+-----+ 540  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGGGAGGGCAGCAG  
a V E W E S N G Q P E N N Y K T T P P V L -  
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
541 -----+-----+-----+-----+-----+-----+-----+ 600  
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC  
a D S D G S F F L Y S K L T V D K S R W Q -

## FIG. 19B

```

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
    .....+.....+.....+.....+.....+.....+.....+
    GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

    AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTGACTTCCTGCCGCACTAC
661 .....+.....+.....+.....+.....+.....+.....+ 720
    TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCACTGAAGGACGGCGTGATG

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  D  F  L  P  H  Y  -

                                BamHI
                                |
    AAAAACACCTCTCTGGGTCACCGTCCGTAATGGATCC
721 .....+.....+.....+.....+.....+.....+ 757
    TTTTGTGGAGAGACCCAGTGGCAGGCATTACCTAGG

a      K  N  T  S  L  G  H  R  P  *
```

## FIG. 20A

NdeI  
|  
CATATGGACTTCCTGCCGCACTACAAAAACACCTCTCTGGGTACCGTCCGGGTGGAGGC  
1 .....+.....+.....+.....+.....+.....+.....+ 60  
GTATACCTGAAGGACGGCGTGATGTTTTTGTGGAGAGACCCAGTGGCAGGCCACCTCCG  
a M D F L P H Y K N T S L G H R P G G G -  
GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG  
61 .....+.....+.....+.....+.....+.....+.....+ 120  
CCACCCCTGTTTGTAGTGTGTACAGGTGGAACGGGTCTGGACTTGAGGACCCCCCTGGC  
a G G D K T H T C P P C P A P E L L G G P -  
TCAGTTTTCTCTTCCCCCAAACCCAAAGGACACCCTCATGATCTCCCGACCCCTGAG  
121 .....+.....+.....+.....+.....+.....+.....+ 180  
AGTCAAAAGGAGAAGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
181 .....+.....+.....+.....+.....+.....+.....+ 240  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
241 .....+.....+.....+.....+.....+.....+.....+ 300  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG  
a V D G V E V H N A K T K P R E E Q Y N S -  
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
301 .....+.....+.....+.....+.....+.....+.....+ 360  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAA  
361 .....+.....+.....+.....+.....+.....+.....+ 420  
ATGTTTACGTTCCAGAGGTTGTTTCGGGAGGGTCTGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
421 .....+.....+.....+.....+.....+.....+.....+ 480  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
481 .....+.....+.....+.....+.....+.....+.....+ 540  
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCTGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG  
541 .....+.....+.....+.....+.....+.....+.....+ 600  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGTGATGTTCTGGTGGGAGGGCAGCAG  
a V E W E S N G Q P E N N Y K T T P P V L -



## FIG. 20B

```
601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAG 660
-----+-----+-----+-----+-----+
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTC

a   D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 720
-----+-----+-----+-----+-----+
GTCCCCCTTG CAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a   Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCCGCGG 761
-----+-----+-----+-----+-----+
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGGCGCC

a   K S L S L S P G K *
```

## FIG. 21A

NdeI  
|  
CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTTCGAGGCCTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

TCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  
61 -----+-----+-----+-----+-----+-----+-----+ 120  
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
121 -----+-----+-----+-----+-----+-----+-----+ 180  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
181 -----+-----+-----+-----+-----+-----+-----+ 240  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC

a V D G V E V H N A K T K P R E E Q Y N S -

ACGTACCGTGTGGTCAGCGTCCCTCACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
241 -----+-----+-----+-----+-----+-----+-----+ 300  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCCTGACCGACTTACCGTTCCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA  
301 -----+-----+-----+-----+-----+-----+-----+ 360  
ATGTTACAGTTCAGAGGTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
361 -----+-----+-----+-----+-----+-----+-----+ 420  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

ACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
421 -----+-----+-----+-----+-----+-----+-----+ 480  
TGTTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG  
481 -----+-----+-----+-----+-----+-----+-----+ 540  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGCACGAC

a V E W E S N G Q P E N N Y K T T P P V L -

GACTCCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
541 -----+-----+-----+-----+-----+-----+-----+ 600  
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

## FIG. 21B

```

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTTCGAATGGACCCCGGGT
-----+-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAAAGCTTACCTGGGGCCCA

a      K  S  L  S  L  S  P  G  K  G  G  G  G  G  F  E  W  T  P  G  -

                                     BamHI
                                     |
721 TACTGGCAGCCGTACGCTCTGCCGCTGTAATGGATCCCTCGAG
-----+-----+-----+-----+-----+ 763
ATGACCGTCGGCATGCGAGACGGCGACATTACCTAGGGAGCTC

a      Y  W  Q  P  Y  A  L  P  L  *
```

## FIG. 22A

NdeI  
|  
CATATGTTTGAATGGACCCCGGGTTACTGGCAGCCGTACGCTCTGCCGCTGGGTGGAGGC  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
GTATACAAGCTTACCTGGGGCCCAATGACCGTCGGCATGCGAGACGGCGACCCACCTCCG  
a M F E W T P G Y W Q P Y A L P L G G G -  
GGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGGGGACCG  
61 -----+-----+-----+-----+-----+-----+-----+ 120  
CCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCTGTTGACTTGAGGACCCCCCTGGC  
a G G D K T H T C P P C P A P E L L G G P -  
TCAGTTTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAG  
121 -----+-----+-----+-----+-----+-----+-----+ 180  
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
181 -----+-----+-----+-----+-----+-----+-----+ 240  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
241 -----+-----+-----+-----+-----+-----+-----+ 300  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC  
a V D G V E V H N A K T K P R E E Q Y N S -  
ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG  
301 -----+-----+-----+-----+-----+-----+-----+ 360  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA  
361 -----+-----+-----+-----+-----+-----+-----+ 420  
ATGTTACAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
421 -----+-----+-----+-----+-----+-----+-----+ 480  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC  
481 -----+-----+-----+-----+-----+-----+-----+ 540  
TGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG  
541 -----+-----+-----+-----+-----+-----+-----+ 600  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGGGCACGAC  
a V E W E S N G Q P E N N Y K T T P P V L -

## FIG. 22B

```
601 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
-----+-----+-----+-----+-----+-----+ 660
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a      D S D G S F F L Y S K L T V D K S R W Q -

661 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 720
GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q G N V F S C S V M H E A L H N H Y T Q -

                                     BamHI
                                     |
721 AAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
-----+-----+-----+-----+-----+ 757
TTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG

a      K S L S L S P G K *
```

# FIG. 23A

NdeI  
|  
1 CATATGGACAAAACCTCACACATGTCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCG 60  
-----+-----+-----+-----+-----+  
GTATACCTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGC

a M D K T H T C P P C P A P E L L G G P -

61 TCAGTTTTCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120  
-----+-----+-----+-----+-----+  
AGTCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC

a S V F L F P P K P K D T L M I S R T P E -

121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180  
-----+-----+-----+-----+-----+  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG

a V T C V V V D V S H E D P E V K F N W Y -

181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240  
-----+-----+-----+-----+-----+  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC

a V D G V E V H N A K T K P R E E Q Y N S -

241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300  
-----+-----+-----+-----+-----+  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC

a T Y R V V S V L T V L H Q D W L N G K E -

301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360  
-----+-----+-----+-----+-----+  
ATGTTACAGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT

a Y K C K V S N K A L P A P I E K T I S K -

361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420  
-----+-----+-----+-----+-----+  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC

a A K G Q P R E P Q V Y T L P P S R D E L -

421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480  
-----+-----+-----+-----+-----+  
TGTTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGG

a T K N Q V S L T C L V K G F Y P S D I A -

481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG 540  
-----+-----+-----+-----+-----+  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGGGAGGGCAGCAG

a V E W E S N G Q P E N N Y K T T P P V L -

541 GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600  
-----+-----+-----+-----+-----+  
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTC

a D S D G S F F L Y S K L T V D K S R W Q -

## FIG. 23B

```
601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
-----+-----+-----+-----+-----+
a   Q G N V F S C S V M H E A L H N H Y T Q -
    AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGTGGTGGTGGTGGTGAACCGAACTGTGAC
661 -----+-----+-----+-----+-----+ 720
    TTCTCGGAGAGGGACAGAGGCCCATTTCCACCACCACCACCACAACCTGGCTTGACACTG
a   K S L S L S P G K G G G G G V E P N C D -
                                     BamHI
                                     |
721 ATCCATGTTATGTGGGAATGGGAATGTTTTGAACGTCTGTAACCTCGAGGATCC 773
    TAGGTACAATACACCCTTACCCTTACAAAACCTTGCAGACATTGAGCTCCTAGG
a   I H V M W E W E C F E R L *
```

## FIG. 24A

NdeI  
|  
1 CATATGGTTGAACCGAACTGTGACATCCATGTTATGTGGGAATGGGAATGTTTTGAACGT 60  
-----+-----+-----+-----+-----+-----+-----+  
GTATACCAACTTGGCTTGACACTGTAGGTACAATACACCCTTACCCTTACAAAACCTTGCA  
a M V E P N C D I H V M W E W E C F E R -  
61 CTGGGTGGTGGTGGTGGTGACAAAACCTCACACATGTCCACCGTGCCCAGCACCTGAACCTC 120  
-----+-----+-----+-----+-----+-----+-----+  
GACCCACCACCACCACCCTGTTTTGAGTGTGTACAGGTGGCACGGGTCGTGGACTTGAG  
a L G G G G G D K T H T C P P C P A P E L -  
121 CTGGGGGGACCGTCAGTTTTCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCC 180  
-----+-----+-----+-----+-----+-----+-----+  
GACCCCCCTGGCAGTCAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG  
a L G G P S V F L F P P K P K D T L M I S -  
181 CGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG 240  
-----+-----+-----+-----+-----+-----+-----+  
GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC  
a R T P E V T C V V V D V S H E D P E V K -  
241 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAG 300  
-----+-----+-----+-----+-----+-----+-----+  
AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC  
a F N W Y V D G V E V H N A K T K P R E E -  
301 CAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG 360  
-----+-----+-----+-----+-----+-----+-----+  
GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTCTGACCGAC  
a Q Y N S T Y R V V S V L T V L H Q D W L -  
361 AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAA 420  
-----+-----+-----+-----+-----+-----+-----+  
TTACCGTTCCTCATGTTTCAGTTCAGAGGTTGTTTCGGGAGGGTTCGGGGGTAGCTCTTT  
a N G K E Y K C K V S N K A L P A P I E K -  
421 ACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC 480  
-----+-----+-----+-----+-----+-----+-----+  
TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG  
a T I S K A K G Q P R E P Q V Y T L P P S -  
481 CGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCC 540  
-----+-----+-----+-----+-----+-----+-----+  
GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG  
a R D E L T K N Q V S L T C L V K G F Y P -  
541 AGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACG 600  
-----+-----+-----+-----+-----+-----+-----+  
TCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGTGATGTTCTGGTGC  
a S D I A V E W E S N G Q P E N N Y K T T -



FIG. 24B

```

601 CCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
-----+-----+-----+-----+-----+-----+ 660
GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTC
a   P P V L D S D G S F F L Y S K L T V D K -

661 AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAC
-----+-----+-----+-----+-----+-----+ 720
TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG
a   S R W Q Q G N V F S C S V M H E A L H N -

                                           BamHI
                                           |
721 CACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAACTCGAGGATCC
-----+-----+-----+-----+-----+-----+ 773
GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTGAGCTCCTAGG
a   H Y T Q K S L S L S P G K *
```

## FIG. 25A

NdeI  
|  
CATATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCG  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC  
a M D K T H T C P P C P A P E L L G G P -  
TCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAG  
61 -----+-----+-----+-----+-----+-----+-----+ 120  
AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGCCTGGGGACTC  
a S V F L F P P K P K D T L M I S R T P E -  
GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC  
121 -----+-----+-----+-----+-----+-----+-----+ 180  
CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG  
a V T C V V V D V S H E D P E V K F N W Y -  
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC  
181 -----+-----+-----+-----+-----+-----+-----+ 240  
CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTGC  
a V D G V E V H N A K T K P R E E Q Y N S -  
ACGTACCGTGTGGTCAGCGTCCCTCACCGTCTTGCACCAGGACTGGCTGAATGGCAAGGAG  
241 -----+-----+-----+-----+-----+-----+-----+ 300  
TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTTGACCGACTTACCGTTCTCTC  
a T Y R V V S V L T V L H Q D W L N G K E -  
TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA  
301 -----+-----+-----+-----+-----+-----+-----+ 360  
ATGTTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT  
a Y K C K V S N K A L P A P I E K T I S K -  
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG  
361 -----+-----+-----+-----+-----+-----+-----+ 420  
CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC  
a A K G Q P R E P Q V Y T L P P S R D E L -  
ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC  
421 -----+-----+-----+-----+-----+-----+-----+ 480  
TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG  
a T K N Q V S L T C L V K G F Y P S D I A -  
GTGGAGTGGGAGAGCAATGGGCAGCCGGAACAACACTACAAGACCACGCCTCCCGTGCTG  
481 -----+-----+-----+-----+-----+-----+-----+ 540  
CACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCAGCAG  
a V E W E S N G Q P E N N Y K T T P P V L -  
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG  
541 -----+-----+-----+-----+-----+-----+-----+ 600  
CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCAGTGGCACCTGTTCTCGTCCACCGTC  
a D S D G S F F L Y S K L T V D K S R W Q -

## FIG. 25B

```

601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG
-----+-----+-----+-----+-----+-----+ 660
GTCCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC

a      Q  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  -

661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGGTGGAGGTGGTGGTTGCACCACCCACTGGGGT
-----+-----+-----+-----+-----+ 720
TTCTCGGAGAGGGACAGAGGCCCATTTCCACCTCCACCACCAACGTGGTGGGTGACCCCA

A      K  S  L  S  L  S  P  G  K  G  G  G  G  G  C  T  T  H  W  G  -

          BamHI
          |
721 TTCACCCTGTGCTAATGGATCCCTCGAG
-----+-----+-----+-----+ 748
AAGTGGGACACGATTACCTAGGGAGCTC

a      F  T  L  C  *
```

# FIG. 26A

NdeI  
|  
CATATGTGCACCACCCACTGGGGTTTCACCCTGTGCGGTGGAGGCGGTGGGGACAAAGGT  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
GTATACACGTGGTGGGTGACCCCAAAGTGGGACACGCCACCTCCGCCACCCCTGTTTCCA

a M C T T H W G F T L C G G G G G D K G -

GGAGGCGGTGGGGACAAACTCACACATGTCCACCTTGCCCAGCACCTGAACTCCTGGGG  
61 -----+-----+-----+-----+-----+-----+-----+ 120  
CCTCCGCCACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTGCTGGACTTGAGGACCCC

a G G G G D K T H T C P P C P A P E L L G -

GGACCGTCAGTTTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGACC  
121 -----+-----+-----+-----+-----+-----+-----+ 180  
CCTGGCAGTCAAAGGAGAAGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGG

a G P S V F L F P P K P K D T L M I S R T -

CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC  
181 -----+-----+-----+-----+-----+-----+-----+ 240  
GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG

a P E V T C V V V D V S H E D P E V K F N -

TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTAC  
241 -----+-----+-----+-----+-----+-----+-----+ 300  
ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG

a W Y V D G V E V H N A K T K P R E E Q Y -

AACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGC  
301 -----+-----+-----+-----+-----+-----+-----+ 360  
TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG

a N S T Y R V V S V L T V L H Q D W L N G -

AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATC  
361 -----+-----+-----+-----+-----+-----+-----+ 420  
TTCTCATGTTTCAGTTCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG

a K E Y K C K V S N K A L P A P I E K T I -

TCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAT  
421 -----+-----+-----+-----+-----+-----+-----+ 480  
AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTA

a S K A K G Q P R E P Q V Y T L P P S R D -

GAGCTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC  
481 -----+-----+-----+-----+-----+-----+-----+ 540  
CTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTG

a E L T K N Q V S L T C L V K G F Y P S D -

ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCC  
541 -----+-----+-----+-----+-----+-----+-----+ 600  
TAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGGGAGGG

a I A V E W E S N G Q P E N N Y K T T P P -

## FIG. 26B

```

601 GTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG
-----+-----+-----+-----+-----+-----+ 660
CACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCC
a      V L D S D G S F F L Y S K L T V D K S R -
      TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
661 -----+-----+-----+-----+-----+-----+ 720
ACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG
a      W Q Q G N V F S C S V M H E A L H N H Y -
                                     BamHI
                                     |
      ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATAATGGATCC
721 -----+-----+-----+-----+-----+ 763
TGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG
a      T Q K S L S L S P G K *
```